June 15, 2002, 09:52:04; Search time 1902.97 Seconds (without alignments) 1971.736 Million cell updates/sec

Run on:

Title: Perfect score: US-09-445-362B-6
278
1 gccaacacgcantccgacga.....cattttnaactcccaggacc 278

Scoring table: Sequence: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : EST:* 1: em_ 2: em_ em_estba:*
em_esthum:*
em_estin:* gb_est1:*
gb_est2:*
gb_htc:*
gb_gss:* em_estmu:*
em_estov:*
em_estpl:*
em_estro:* em_gss_hum:*
em_gss_inv:*
em_gss_pln:*
em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	17	16	15	c 14	13	c 12	11	10	9	œ	7	6	ი 5	4	ω	2	1	Result No.
	112.4	115.6	115.6	115.6	120	131.2	137.2	141	145	145.6	149	150.4	150.4	193	203	214.4	257.8	Score
•	40.4	41.6	41.6	41.6	43.2	47.2	49.4	50.7	52.2	52.4	53.6	54.1	54.1	69.4	73.0	77.1	92.7	Query Match Length
	337	1635	960	407	638	518	538	938	309	616	608	593	459	468	416	477	279	Length
	10	11	9	10	10	12	10	10	10	w	10	ø	12	10	10	S	10	DB
	BG979894	AK017072	AV254558	BE988123	BJ068008	AQ311743	BF140778	B1853762	C04505	AA881875	BF454139	AA624918	AZ985110	W12756	BF543291	AI327454	C04498	ID
	BG979894 PM2-CN009	AK017072 Mus muscu	AV254558 AV254558	BE988123 UI-M-CG0p	800890rg 800890rg	AQ311743 RPCI11-10	BF140778 601788336	BI853762 603380312	C04505 C04505 Huma	AA881875 vx29a04.r	BF454139 maa10c03.	AA624918 vn90e12.r	AZ985110 2M0266C19	W12756 ma68a06.rl	BF543291 UI-R-Y0-a	AI327454 ma68a06.y	C04498 C04498 Huma	Description

BASE COUNT ORIGIN

Query Match

92.7%;

Score 257.8; DB 10; Length 279;

	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	C04498	RESULT 1	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.	EST.	C04498.1 GI:1467749	C04498	3NHC3467, mRNA sequence.	C04498 Human heart cDNA (YNakamura) Homo sapiens cDNA clone	C04498 2			
ta; Craniata;							Nakamura) Homo	279 bp mRNA			
/ertebrata;							sapiens cD	linear			
Euteleostomi;			•)			NA clone	linear EST 30-JUL-1996			
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ALIGNMENTS

ORIGIN	BASE COUNT			•					source	FEATURES							COMMENT	MEDLINE	JOURNAL		TITLE		AUTHORS	REFERENCE		
	79 a	from adult heart"	<pre>/note="Organ: heart; normalized directionally cloned cDNA</pre>	/dev_stage="adult"	/clone_lib="Human heart cDNA (YNakamura)"	/clone="3NHC3467"	/db_xref="taxon:9606"	/organism="Homo sapiens"		Location/Qualifiers	Email: yusuke@ims.u-tokyo.ac.jp.	Fax: 81-3-5449-5433	Tel: 81-3-5449-5372	4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan	University of Tokyo	Institute of Medical Science	Contact: Yusuke Nakamura	96299762	Genomics 35 (1), 231-235 (1996)	adult heart and analysis of 3040 clones by partial sequencing	Construction of a normalized directionally cloned cDNA library fr	Nakamura, Y.	Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and	1 (bases 1 to 279)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	

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RESULT
AI327454
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JOURNAL
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nes 275; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
Contact: Marra MyMouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMAN);, mRNA sequence.
AI327454
                                                                                                                                                                                                                                                                                                                                                                                                                                       This read is a RESEQUENCE of a prev
This read has been verified (found
correct orientation)
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina

1 (bases 1 to 477)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Moore, B.

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1327454
477 bp mRNA linear EST 23-DEC ma68a06.yl Soares mouse p3NMF19.5 Mus musculus cDNA clone mAGE:315826 5' similar to gb:X54162_rna1 64 KD AUTOANTIGEN D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMACE Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:206442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R.
The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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Query Match Best Local S Matches 236 339 241 181 159 279 121 219 61 99 ctnctgaggctgggntaccattttnaactcccaggacc 278 cacatcatgggcagccaggtggaaatggagattgtcaagctnctgaaggagaacacgacg atcatgagagctctccagcacaacacggtgctcacggagctgcggtttcataaccagagg CTGCTGAGGCTGGGCTACCATTTTGAGCTCCCAGGACC CACATCATGGGCTCTCAGGTGGAGATGGAAATTGTCAAGCTGCTCAAAGAGAATACCACG GCCAACACGCACGCTGATGACGCCGCGGCGATTGCCATTGCAGACATGCTCAAGGTTAAC 158 gccaacacgcantccgacgacagtgcagccatggtcattgcagagagatgcncaaagtcaat 60 ATCATGAGAGCCCTGCAGCACAACACGGTGCTCCACGAGCTGCGCTTCCACAACCAGCGG al Similarity 236; Conserv 147 Conservative a adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pm773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)." 77.1%; 84.9%; 0 Score 214.4; DB 9; Pred. No. 4.6e-43; 0; Mismatches 42; 376 Indels Length 477; 0; Gaps 240 180 278 0,

ACCESSION VERSION KEYWORDS JOURNAL MEDLINE COMMENT REFERENCE AUTHORS SOURCE ORGANISM DEFINITION source Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Lowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
7el: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID- 1790895 BF543291 416 bp mRNA linear UI-R-Y0-abd-c-03-0-UI.rl UI-R-Y0 Rattus norvegicus UI-R-Y0-abd-c-03-0-UI 5', mRNA sequence. 97044477 Seq primer: M13 Forward discovery 1 (bases 1 to 416)

Bonaldo, M.F., Lennon, G. and Sor

Normalization and subtraction: Eukaryota; Metazoa; Mammalia; Eutheria; Norway rat. Rattus norvegicus BF543291 BF543291.1 GI:11634398 Rattus /organism="Rattus norvegicus" /strain="Sprague-Dawley" /db_xref="taxon:10116" /clone="UI-R-Y0-abd-c-03-0-UI" /clone_lib="UI-R-Y0" Socation/Qualifiers Lennon, G. and Soares, M.B. 791-806 (1996) Chordata; Rodentia; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; two approaches 6 facilitate gene 11-DEC-2000 clone

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*on *Jun
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Query Match Best Local 121 atcatgagagctctcccagcacaacacggtgctcacggagctgcggtttcataaccagagg 212 GAGCACATTACCAGCGTAAACGTGGAGTCCAACTTCATCACCGGGAAGGGGATCCTGGCC 332 CACATCATGGGCTCCCAGGTCGAGATGGAGATTGTCAACCTGCTCAAGGAGAATACCACG 181 cacatcatgggcagccaggtggaaatggagattgtcaagctnctgaaggagaacacgacg 272 ATCATGAGAGCGCTGCAGCACAACACAGTGCTCACCGAGCTGCGCTTCCACAACCAGAGG 152'-GCCAACACGCACGCTGACGACGCCGCGGCGATTGCCATTGCGGAAATGCTCAAGGTTAAC 61 gagcacatcaccaacgtaaacgtcgagtccaacttcataacgggaaaggggatcctggcc 120 1 gccaacacgcantccgacgacagtgcagccatggtcattgcagagatgcncaaagtcaat 60 ctnctgaggctgggntaccatttt 264 CTGCTGAGGCTGGGCTACCATTTT 415 224; w12756 468 bp mRNA linear EST 02-OCT ma68a06.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:315826 5' similar to gb:X54162_rnal 64 KD AUTOANTIGEN D1 Mus musculus Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 468)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kuada,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and W12756.1 GI:1286794 (HUMAN);, mRNA sequence. W12756 Similarity house mouse. 123 Conservative /dev_stage="adult"
//lab_host="pHiOB_(Life Technologies)"
//lab_host="pHiOB_(Life Technologies)"
//lab_host="pHiOB_(Life Technologies)"
//lab_host="pHiOB_(Life Technologies)"
//lab_host="pMiOB_(Life Technologies)"
//lab_host="pMiOB_Pac (Pharmacia) with a modified
//lab_host="pMiOB_Pac (Pharmacia) with a modified whole-eye library in
//lab_host="pMiOB_Pac (Pharmacia) with the normalized whole-e bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B 112 c 73.0%; 0; Score Pred. 105 g Mismatches 203; DB 10; No. 2.9e-40; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus 40; Length 416; Indels EST 02-OCT-1997 0; Gaps 240 180 211 271 391 331 Mus. 0;

BASE COUNT ORIGIN

Matches

ACCESSION VERSION

SOURCE KEYWORDS

ORGANISM

REFERENCE

AUTHORS

Waterston, R

WashU-HHMI Mouse

EST

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RESULT W12756

DEFINITION

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Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: mob.REGA+ET
High quality sequence stop: 403
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the LLAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WashU-HHMI Mouse EST Project
Washington University School of MedicineP
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                  GSS.
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AZ985110.1
                                                                                                                            AZ985110 459 bp DNA linear GSS 27-APK-20
2M0266C19R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
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118 c 120 g 85 t 1 others
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/dev_stage="19.5 dpc total fetus"
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Pred. No. 8.9e-38;
0; Mismatches 41;
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  218 CACATCTGTGGGGGCAAGACTGAGATGGAGATCGCCAAGCTGCTCAAGGAGAACACCACC
                      181 cacatcatgggcagccaggtggaaatggagattgtcaagctnctgaaggagaacacgacg
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                                                                                                   atcatgagagctctccagcacaacacggtgctcacggagctgcggtttcataaccagagg
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                                                                                                                                                                                  ATCTTCCGGGCCCTCCTCCAGAACACACTCTGACAGAGCTGCGCTTTCACAACCAGAGG
                                                                                                                                                           AAGACCATCACCAGCCTCAACCTGGACTCCAATCACATCACTGGCCAAAGGCATCCTGGCC
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Res
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Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0266 row: C column: 19
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb)AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0266C19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. coli strain XL10-Gold, T1-resistant,
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121 atcatgagageteteeageaeaeaeaeggtgeteaeggagetgeggttteataaeeagagg 180
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
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/dev_stage="13 day embryos"
/lab_host="SoLr (kanamycin resistant)"
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Vector: pBluescript Steel"
/note="Organ: heart; Vector: pBluescript St.; Site_1:
/note="Organ: heart; Vector: pBluescript St.; Site_1: heart; Vector: pBluescript St.; Site_1:
/note="Organ: heart; Vector: pBlue
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/clone="IMAGE:1039246"
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/strain="NIH/Swiss"
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AAC40660	AAZ49560	AAX58276	ABL14346	ABL14342	ABL14347	ABL14343	AAH89247	AAH07715	AA168201	AAC81955	AAH18056	AAH89246	ABL20030	ABL02802	AAH52003	AAC50296	AAQ47357	AAT51411	ABL20031	ABL02803	AAC91326	AAC77309	AAI60475	AAI58689	AAH24545	AAH98259	817	331	233	97	799	AAI59784	024	AAA50238	AAK00088
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ALIGNMENTS

RESULT AAC76864

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AAC76864 standard; cDNA; 906

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Human ORFX ORF2419 polynucleotide sequence SEQ ID NO:4837.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopatho; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antinugal; antithreunatic; antithryoid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss.

31-MAR-2000; 2000WO-US08621.

WO200058473-A2

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2001
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Chen A, D'Sa SA, Amshey S, Dufour GE, Flores V, Fong Liu TF, Roseberry AM, Rose Wright RJ, Yap PE, Yu JY, Hodgson Spiro PA, DM, Banville SC, Shah P, Chaluy ..., shey S, Dahl CR, Dam TC, Daniels SE; Fong WT, Greenawalt LB, Hillman JL, Jc I, Rosen BH, Russo FD, Stockdreher TK, I Yu JY, Bradley DL, Bratcher SR, Chen W; Lincoln SE, Jackson S; Jones P , Daffo SC; O AL;

2001-502867/55. DB; AAU19573.

Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics

Claim 1; Page 372-373; 522pp; English

The invention relates to polynucleotides (I) end therapeutic (DITHP) polypeptides (II), which ind and proteins involved in growth and development encoding diagnostic and include e.g. enzymes, receptors. (I) and

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Copyright (c) 1993 - 2000 Compugen Ltd.
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PCT-US94-04361-25
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US-09-233-752A-19
US-09-402-036-19
US-08-471-044-30
US-08-471-046-30
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Sequence 17,	Sequence 26,	Sequence 17,	Sequence 26,	Sequence 17,	Sequence 35,	Sequence 35,	Sequence 35,	Sequence 35,	Sequence 35,	Sequence 35,	Sequence 35,	Sequence 1,	Sequence 1,	Sequence 1,	Sequence 13,	Sequence 1,	Sequence 1,	
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ALIGNMENTS

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REFERENCE/DOCKET NUMBER: 96700/238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELLEFAX: (212) 286-0854 or 286-0882
TELLEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
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APPLICANT: William R. Jacobs,
APPLICANT: Barry R. Bloom
APPLICANT: Graham F. Hatfull
  MOLECULE TYPE:
DESCRIPTION:
                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     FILING DATE: February 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: PASQUALIDI, PATTICIA A.
REGISTRATION NUMBER: 34,894
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOCTWARE: WORD PROCESSOR (ASCII)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MYCOBACTERIAL SPECIES-SPECIFIC TITLE OF INVENTION: REPORTER MYCOBACTERIOPHAGES
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                                     TYPE: nucleotide STRANDEDNESS: sir TOPOLOGY: linear
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                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: William R. Jacobs, Jr.
APPLICANT: Barry R. Bloom
APPLICANT: Graham F. Hatfull
TITLE OF INVENTION: MYCOBACTERIAL SPECIES-SPECIFIC
TITLE OF INVENTION: REPORTER MYCOBACTERIOPHAGES
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COMPUTER READABLE FORM:
                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
AUTHORS: Hatfull and Sarkis
TITLE: DNA Sequence, Structure and Gene
TITLE: Expression of Mycobacteriophage 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL TYPE: not applicable
CELL LINE: not applicable
ORGANELLE: not applicable
ORGANELLE: not applicable
IMMEDIATE SOURCE: mycobacteriophage L5 particles
POSITION IN GENOME: entire genome
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INDIVIDUAL ISOLATE: L5
DEVELOPMENTAL STAGE: not app
HAPLOTYPE: not applicable
TISSUE TYPE: not applicable
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                                COUNTRY:
                                                        STATE:
                                                                        CITY: New York
                                                                                        STREET:
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PAGES: 395-405
DATE: 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD: OTHER INFORMATION:
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                                                                                        90 Park Avenue
                                  U.S.A.
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Pred. No. 0.033;
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US-08-705-557-1
                                                                                                                                  Query Match
Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
46824 GTACGTTGCCGCACAAGCGTTGTTGCTGCACGGCATGGCTCAGGCCCTGCACTGCAAGAC 46765
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DESCRIPTION:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL TYPE: not applicable
CELL LINE: not applicable
ORGANELLE: not applicable
IMMEDIATE SOURCE: mycobacteriophage L5 particles
POSITION IN GENOME: entire genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/83
FILING DATE: February 7.
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patrici
                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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PAGES:
                                                                                            27 agccatggtcattgcagagatgcncaaagtcaatgagcacatcaccaacgtaaacgtcga 86
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SOFTWARE: Word Processor (ASCII)
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                                                                                                                                                                                                                                                                                                                                        TITLE:
                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: Hatfull and Sarkis
                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
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REFERENCE/DOCKET NUMBER: 96700/238
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Pred. No. 0.033;
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Maximum Match 100%
Listing first 45 summaries
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                                                                   Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
 Score
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278
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Copyright (c) 1993 - 2000 Comp
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	AC006333 Homo sapi AX002051 Sequence AX002052 Sequence AX002053 Sequence AX002056 Sequence AC103173 Rattus no AF237628 Mus muscu AL513217 Human DNA AC025664 Homo sapi AX329789 Sequence AX331533 Sequence AX331932 Sequence AX331932 Sequence

ALIGNMENTS

RESULT 1
AC006333
LOCUS
DEFINITION
ACCESSION
VERSION REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE JOURNAL REFERENCE AUTHORS TITLE SOURCE ORGANISM KEYWORDS 187532 bp Homo sapiens BAC clone RP11-390E23 AC006333 AC006333.3 GI:5523811 2 (bases 1 to 187532)
Rohlfing,T., Bauer,C. and Ketterman,M.
The sequence of Homo sapiens BAC clone RP11-390E23
Unpublished Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 187532)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998). human. HTG. 3 (bases 1 to 187532) Waterston, R.H. Direct Submission from DNA 7, complete linear sequence. PRI 30-SEP-2000,

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REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
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                                                                                                FEATURES
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                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Jul 17, 1999 this sequence version replaced gi:4454617.
Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence are covered by sequence than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                              The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tachen, M., Catanese, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
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Direct Submission
Submitted (17-JUL-1999) Genome Sequencing Center, Washington
Submitted (17-JUL-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-JAN-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
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                                                                                                                   hindiii in the real fragment digest. according to the restriction digests
                                                                                                                                       The sequence fidelity is in question at base positions 75394-75555 due to a non-perfect GA run. The insilico digest fragments are 3570 for ecorv and 8922 for hindili compared to 3573 for ecorv and 8997 hindili in the real fragment digest. Assembly appears to be correct
                                                                                                                                                                                                                                                         The clone sequenced to the right is a Actual start is at base position 1 of 1716 of GSI-195F7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.
                                                                                                                                                                                                                                                                                                                                NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          (http://bacpac.med.buffalo.edu)
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Contact: sapiens@watson.wustl.edu
Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center Center code: WUGSC
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
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8101. .8622
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190. .231
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2. .182
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Q9bufl homo sapien
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Q9ny19 homo sapien
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Q9dea6 gallus gall
Q9jhj0 mus musculu
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P70566 rattus norv
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ALIGNMENTS

RESULT Q99PM7

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Matches 301; Conserv
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                      Conley C.A., Fritz-Six K.L., Almenar-Queralt A., Fowler V.M.
"Leiomodins: larger members of the tropomodulin (tmod) gene
Genomics 73:127-139(2001).

EMBL; AF237628; AAK00789.1; -.
MGD; MGI:2135672; Lmod2.
NON_TER 1
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SEQUENCE 333 AA; 37463 MW; F082494410157A31 CRC64;
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
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                                                        NVESNFITGKGILAIMRALQHNTVLTELRFHNQRHIMGSQVEMEIVKLLKENTTLLRLGY 333
HFELPGPRMSMTSILTRNMDKQRQKRLQEQKQQEGYDGGPNLRTKVWQRGTPSSSPYVSP
                                         NVESNFITGKGILAIMRALQHNTVLTELRFHNQRHIMGSQVEMEIVKLLKENTTLLRLGY 123
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Pred. No. 1.4e
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Best Local s
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    Q9JKK7
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Submitted (OCT-201) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria;
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Primates;
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40194 MW;
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Pred. No. 2.3e-29;
3; Mismatches 102;
  PRT;
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Best Local Similarity
Matches 148; Conserv
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Q1-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, L
01-JUN-2001 (TrEMBLrel. 17, L
NEURAL TROPOMODULIN N-TMOD.
                                                                                             01-FEB-1997
01-FEB-1997
01-JUN-2001
                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                            P70566;
 SEQUENCE FROM N.A. STRAIN-SPRAGUE-DAWLEY; MEDLINE-97041709; PubM
                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                  N-TROPOMODULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Conley C.A., Almenar-Queralt A., "Identifying novel tropomodulin: "Identifying novel tropomodulin biol. Cell 9:18A-18A(1998). [2]
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                            (TrEMBLrel.
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                                                                                                                                       PRELIMINARY;
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WLEY; TISSUE=BRAIN;
PubMed=8886980;
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Pred. No. 3.
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                                                 Craniata; Veri
Sciurognathi;
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                                                             Vertebrata; Euteleostom1;
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OM protein - protein search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

June 13, 2002, 09:45:55; Search time 13.45 Seconds (without alignments) 1589.085 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-445-362B-4 2839

1 MSTFGYRRGLSKYESIDEDE.....SIKQLKRVEVPEALRWEHDL 552

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

105224

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	-!- DISEASE: RECOGNIZED BY PATIENTS WITH AUTOIMMUNE THYROID DISEASE. -!- SIMILARITY: BELONGS TO THE TROPOMODULIN FAMILY.	 -I- SUBCELLULAR LOCATION: CYTOSKELETON. -I- TISSUE SPECIFICITY: SMOOTH MUSCLE (HEART, SKELETAL MUSCLE, COLON AND SMALL INTESTINE), A SUBSET OF STRIATED MUSCLE FIBERS, AND AT LOW LEVEL IN THYROID. 	onley C.A., Fritz-Six K. Leiomodins: larger membe enomics 73:127-139(2001)	CHARACTERIZATION. CHARACTERIZATION. MEDLINE-21218919; PubMed=11318603;	Leromourn and tropomountin in smooth muscle."; Am. J. Physiol. 280:C1645-C1656(2001).		CHARACTERIZATION. MEDLING-21240187: PubMed-11350761:	Res. 19:313-322(1999).	"Localization of the human 64kD autoantigen D1 to myofibrils in a subset of extraocular muscle fibers.";		IZATION.	J. Clin. Endocrinol. Metab. 72:1375-1381(1991).	"Cloning and sequencing of a novel 64-kDa autoantigen recognized by patients with autoimmune thyroid disease.";	Ludgate M., Vassart G.;	TISSUE-Thyroid;	ACCUPATION OF THE PROPERTY OF	Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.	apiens (Human). ota: Motazoa: Chordata: Craniata: Vertebrata:	ophthalmopathy autoantigen) (Smooth muscle leiomodin) (SM-Lmod). LMOD1.	(Leiomodin, mu	<pre>01-APR-1993 (Rel. 25, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)</pre>	(Rel. 25,	

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PIR; S26815; S26815.
MIM; 602715; ...
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tropomodulin - mouse
C;Specias: Mus sp. (mouse)
C;Date: 02.Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
C;Accession: I53091
R;Ito, M.; Swanson, B.; Sussman, M.A.; Kedes, L.; Lyons, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: modulates the C; Superfamily: tropomodulin C; Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:S76831; NID:g914213; C;Genetics: A;Gene: Imod C;Function:
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A;Title: Cloning of tropomodulin cDNA and localization of gene transcripts during mouse
A;Reference number: I53091; MUID:95154574
A;Accession: I53091
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iol. 167, 317-328, 1995
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                                                                                                  LTRFAEALKONTVVKTFSLANTHADDSAAMAIAEMLKANEHITNVNVESNFITGKGILAI 288
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tyopomodulin, skeletal muscle - chicken
¿:Species: Gallus gallus (chicken)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 22-Jun-1999
C:Accession: A55463
R;Babcock, G.G.; Fowler, V.M.
R;Babcock, G.G.; Fowler, V.M.
                                  C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
C;Accession: A42336
R;Sung, L.A.; Fowler, V.M.; Lambert, K.; Sussman, M.A.; Karr, D.
J Biol. Chem. 267, 2616-2621, 1992
A;Title: Molecular cloning and characterization of human fetal 1
A;Reference number: A42336; MUID:92129352
A;Accession: A42336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 269, 27510-27518, 1994
A;Title: Isoform-specific interaction of tropomodulin with skeletal muscle and erythr A;Reference number: A55463; MUID:95050495
A;Accession: A55463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-359 <BAB>
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A; Molecule type: mRNA
A; Residues: 1-359 <SUN>
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Best Local
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%%; Pred. No. 4.8e-23;
63; Mismatches 117;
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2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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(without alignments)
922.856 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
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  Length
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1 US-08-899-595-3

2 US-09-080-897-2

1 US-09-080-897-2

1 US-09-080-897-4

2 US-09-227-420-1

2 US-09-227-420-1

2 US-09-227-420-1

2 US-09-08-237-35-2

1 US-09-041-886-2

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2 US-09-041-886-31

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6 US-09-041-886-31

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       Query Match
Best Local Similarity
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Result No.

151 5.3 3119 1 US-U8-433-203-10 149.5 5.3 905 2 US-08-574-959A-9 149.5 5.3 1135 2 US-08-574-959A-7 149.5 5.3 1135 2 US-08-574-959A-7 149.5 5.3 1135 2 US-09-357-014-9 149.5 5.3 1135 4 US-09-357-014-7 149.5 5.3 1135 4 US-09-357-014-7 149 5.2 1958 1 US-07-853-913-2 149 5.2 1958 1 US-07-853-913-2 149 5.2 2441 1 US-08-194-68-2 149 5.2 2441 3 US-08-810-433-2 147 5.2 281 2 US-08-815-190A-2 147 5.2 281 4 US-09-29-640-25 147 5.2 281 4 US-09-29-640-25 147 5.2 281 4 US-09-39-214-8 147 5.2 281 4 US-08-339-214-8 147 5.2 281 5 PCT-US-08-339-214-30 147 5.2 281 5 PCT-US-08-339-214-30 147 5.2 976 4 US-09-104-324B-4	5.2 281 4 5.2 281 4 5.2 281 4 5.2 281 4 5.2 281 4 5.2 281 4 5.2 281 4
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US-08-57-014-9 US-08-57-014-9 US-09-357-014-9 US-09-357-014-7 US-09-29-213B-25 US-07-853-913-2 US-07-945-283-2 US-08-914-468-2 US-08-915-190A-2 US-08-815-190A-2 US-08-815-190A-2 US-08-815-190A-2 US-08-339-214-8 US-08-339-214-8 US-08-339-214-8 US-08-339-214-8 US-08-339-214-8 US-08-339-214-8 US-09-339-214-8 US-09-339-214-8 US-09-339-214-8	Sequence 7 Sequence 7 Sequence 8 Sequence
	10 10 10 10 10 10 10

ALIGNMENTS

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; TOPOLOGY: linear ; ~ MOLECULE TYPE: protein US-08-999-774A-2
                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/999,774A

FILING DATE: 10-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/032,818
FILING DATE: 11-DEC-1996
ATTORNEY/AGENT IMFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34.090
REFERENCE/DOCKET NUMBER: DX0646
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                             TELEFAX: (650)496-120 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lees, Emma M.
APPLICANT: McClanahan, Terrill K.
APPLICANT: McClanahan, Terrill K.
TITLE OF INVENTION: Intracellular Regulatory Molecules;
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1105 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 901 California Avenue CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Application US/08999774A 6274312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     California
                                                                        amino acid
                                                                                                   1105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gish, Kurt C.
Seghezzi, Wolfgang
Shanahan, Frances
                                                                                                                                                                   (650)496-1200
                                                                                                                                                2
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6.9%;

Score 197; DB 4; Pred. No. 1e-05;

Length 1105;

Matches

99;

716

7

26;

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Sequence 3, Application US/08899595 Patent No. 6111072
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Flopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                        FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NATUMIYA, Shuh
APPLICANT: TAKAHASHI, NO. 6111072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND
TITLE OF INVENTION: ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1083 PPPPPADGVPPPPAP 1097
                     APPLICATION NUMBER: JP 9-90170 FILING DATE: 25-MAR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1024 MPGQHMPGRMIPTVAAN-IHPSGSGPTPPGMPPMPGNILGPRVPLTAPNGMYPPPPQQQP 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             440 PPPPP----PPPPLP 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 QEQKQQEGYDGGPNLRTKVWQRGTPSSSPYVSPRHSPWSSPKLP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 FSLANTHADDSAAMAIAEMLKANEHITNVNVESNFITGKGILAIMRALQHNTVLTELR-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 SQEEEEEEDSDEEERTIETAKGINGTVNYDSVNSDNSKPKIFKSQIENINLINGSNGRNT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      769 EPEKL----EGAEEEKMEADPDGQQPEKAENKVENETD-----EGDKAQDGENEKNSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 SREALMAYWEKESQKLLEKERLGECGKVAEDKEESEEELIFTESNSEVSEEVYTEEEEEEE 124
                                                                                                                                                                                                APPLICATION NUMBER: US/08/899,595 FILING DATE: 24-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HNQRHIMGSQ---VEMEIVKLLKENTTLLRLGYHFELPGPRMSMTSILTRNMDKQRQKRL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QNPQQAHQHSGGPGL-APLGAAGHPGMMPHQQPPPYPLMHQMPPPHPPQPGQIPGPGSM 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EELETIMDREKEALEQORQOLLTE----RONFHME----QLKYAELRARQOMEQQQHG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -EISEGNVATAAAAALASAATKAKHL--AAVEERKI--KSLVALLVETQMKKLEIKLRHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESPAAIHPCGNPTVIEDALDKIKSNDPDTTEVNLNNIENITTQTLTRFAEALKDNTVVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQDSEVSEDTKSEEKETE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAALEEFSRVREEVPLELVEAHVKKVQEAARASGKVDP----TYGLESSCI----AGTGPD 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRGLSKYESIDEDELLASLSA--EELKELERELEDIEPDRNLPVGLRQKSLTEKTPTGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KKVQTVRSRPLSPVATLPPPPPPPPPPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Foley & Lardner 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                   JP 8-242701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suite 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1315 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                     Sequence 2, Applic
Patent No. 5985574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.4%; Score 182.5; DB 3; Best Local Similarity 22.0%; Pred. No. 0.00013; Matches 116; Conservative 70; Mismatches 174;
                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: King, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                               NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                            APPLICANT: MOTTOW, Jan E. APPLICANT: Welcsh, Piri L. APPLICANT: Leon, Pedro E. TITLE OF.INVENTION: Modula
                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                         705
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  STREET:
CITY: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 IDEDELLASL----SAEELKE-----LER-ELEDIEPDRNLPVGLRQKSLTEKTPTGTF 64
                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                         GIPSPSSLPGGTAIPPPPPLPGSARIPPPPPPLPGSAGIPPPPPPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIENITTQTLTRFAEALKDNTVVKTFSLANTHADDSAAMAIAEMLKANEHITNVNVESNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLINALITPAEELDFRVHIRSELMRLGLHQVLQDLREIENE-----DMRVQLNVFDEQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----TPPPPPPPPPPPPPLPGGVCISSPPSLPGGTAISPPPPLSGDATIPPPPPLPEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K-----ELEDAKKEMASLSAAAITVPPSVPSRAPVPPAPPLPGDSGTIIPPPPAPGDST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLGYHFELPGPRMSMTSI----LTRNMDKQRQKRLQEQKQQEGYDG------GPNLRTK 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TARHELQVEMKKMESDFEQKLQDLQGEKDALHSEKQQIATEKQDLEAEVSQLTGEVAKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITGKGILAIMRALQHN--TVLTELR-----FHNQRHIMGSQ---VEMEIVKLLKENTTLL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YYK-----LIEECISQIVLHKNGADPDFKCRHLQI 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IFKSQIENINLTNGSNGRNTESPAAIHPCGNPTVIEDALDKI----KSNDPDTTEVNLN- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEDSYDLKGRLDDIRMEMDDFNEVFQILLNTVKDSKAEPHFLSILQHLLLVRNDYEARPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEESQE-----EEEEEDSDEE-ERTIETAKGINGTVNYDSV------NSDNSKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SR-EALMAYWEKESQKLLEKERLGECG--KVAEDKEESEEELIFTESNSEVSEEVYTEEE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDAAKLLSALCILPQPEDMNERVLEAMTERAEMDEVERFQPLLDGLK-SGTTIALKVGCL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VWQRGTPSSSPYVSPRHSPW------SSPKLPKKVQTVRSRPLSPVATLPPPPPP-----
SSEE: SCIENCE & TECHNOLOGY LAW GROUP
T: 75 DENISE DRIVE
HILLSBOROUGH
                                                                                                                                                                                                                                                                                                          Application US/09080897
                                                                                                                                                                                                Lynch, Eric D.
Lee, Ming
                                                                                                                                                                                                                                             King, Mary-Claire
                                                                                                            Modulators
                                                                                       14
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ER: 049441/0112
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                                                                                                                                                                                                                                                                                                                                                                                                                           751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    649
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US-08-899-595-3

GENERAL INFORMATION:

STREET: 3000 K St CITY: Washington STATE: D.C.

ADDRESSEE:

COUNTRY:

USA

20007-5109

CLASSIFICATION:

Stephen

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Result
No.
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
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                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                 2839
2063.5
1447
    650.5
613
                                            964
963
779.5
709.5
705
                                                                                                                                                                                                                                                         Score
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1: /SIDS1/gcgdata/h
2: /SIDS1/gcgdata/h
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5: /SIDS1/gcgdata/h
6: /SIDS1/gcgdata/h
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22: /SIDS1/gcgdata/
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length: 2000000000
    100.0
100.0
72.7
51.0
34.0
33.9
27.5
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Human polypeptide
Human polypeptide
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Human DCMAG-1 prot
Human diagnostic a
Human ORFX ORF2419
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Arabidopsis	AAG24963	22		0 0	180.5	4 3
Human ORFX ORF338	AAB40574	21	2518	6.4	181	42
Human secre	AAG00851	21	100		182	41
	AAW76734	20	1315		182.5	40
Human 07CG27 gene	AAB35408	22	2819		183.5	9 0
Drosophila melanoq	ABB67210	22	3263		184	ب م
Human brain expres	UVEBSME) i	748		100	1 C
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Green Huorescent	AAW85034	19	635		187	34
Drosophila melanog	ABB64608	22	1700		193	\mathfrak{S}
Shrimp white spot	AAG85017	22	757		193.5	32
Drosophila melanog	ABB60327	22	3111		194.5	31
Mouse JMY protein	AAY09513	20	983		194.5	30
Drosophila melanog	ABB58220	22	527	•	195.5	29
Human intracellula	AAE09325	22	1105		197	28
Drosophila melanog	ABB62516	22	1162	7.0	198.5	27
Human protein sequ	AAB95239	22	560	•	211.5	26
Shrimp white spot	AAG85039	22	1174	8.0	226	25
Human polypeptide	AAM40352	22	1017	•	240.5	24
Novel human secre	AAU30835	22	141	•	348	23
Human polypeptide	AAO11834	22	273	12.7	360	22
Drosophila melanog	ABB58218	22	403	•	374	21
Drosophila melanog	АВВ66832	22	367	•	374	20
Human protein sequ	AAM25794	22	174	•	376	19
Human heart muscle	AAW90173	20	92	•	378	18
Human protein SEQ	AAM80185	22	223	•	416	17
Human cardiovascul	AAU21876	22	104	•	480	16
Novel human secre	AAU30836	22	391	•	553.5	15
Human ORFX ORF2864	AAB43100	21	368	•	561	14
Human polypeptide	AAM41319	22	358	21.6	61,3	13
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ALIGNMENTS

AAW90172 RESULT

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AAW90172 standard;

Protein;

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16-MAR-1999 AAW90172;

(first entry)

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PSXXX
                                                                                                                                                                                                                                Human heart muscle specific protein
Claim 1; Fig 4; 58pp; German
                New nucleic acid selectively expressed in insufficient cardiac muscle - for treatment and diagnosis of heart disease
                                             WPI; 1999-060330/05.
N-PSDB; AAV74263, AAV74264, AAV74365.
                                                                        Domdey H, Henkel T,
                                                                                          (MEDI-) MEDIGENE AG.
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                                                                                                                                                                                     Homo sapiens
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Matches 552
       DCMAG-1; human; dilative cardiomyopathy; cardiac muscle cell; cardioactive agent; heart disease; treatment.
                                         Human DCMAG-1 protein
                                                              06-SEP-2001
                                                                                   AAB86278
                                                                                                         AAB86278
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New pathologically altered cardiomyocyte, useful for identifying and detecting cardioactive agents, produced by stimulating healthy cells with hormones and cytokines \, -
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                                  QEQKQQEGYDGGPNLRTKVWQRGTPSSSPYVSPRHSPWSSPKLFKKVQTVRSRPLSFVAT
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